



SEQUENCE LISTING

<110> DARST, SETH A.
CAMPBELL, ELIZABETH

<120> A CRYSTAL OF BACTERIAL CORE RNA POLYMERASE WITH
RIFAMPICIN AND METHODS OF USE THEREOF

<130> IPT-012.02

<140> 10/783,206
<141> 2004-02-20

<150> 09/802,755
<151> 2001-03-09

<160> 30

<170> PatentIn Ver. 3.2

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35 40 45
Ile Phe Gly Pro Ile Lys Asp Tyr Glu Cys Ala Cys Gly Lys Tyr Lys
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Arg Gln Arg Phe Glu Gly Lys Val Cys Glu Arg Cys Gly Val Glu Val
65 70 75 80
Thr Arg Ser Ile Val Arg Arg Tyr Arg Met Gly His Ile Glu Leu Ala
85 90 95
Thr Pro Ala Ala His Ile Trp Phe Val Lys Asp Val Pro Ser Lys Ile
100 105 110
Gly Thr Leu Leu Asp Leu Phe Ala Thr Glu Leu Glu Gln Val Leu Tyr
115 120 125
Phe Asn Lys Tyr Ile Val Leu Asp Pro Lys Gly Ala Val Leu Asp Gly
130 135 140

Val	Pro	Val	Glu	Lys	Arg	Gln	Leu	Leu	Thr	Asp	Glu	Glu	Tyr	Arg	Glu	145	150	155	160
Leu	Arg	Tyr	Gly	Lys	Gln	Glu	Thr	Tyr	Pro	Leu	Pro	Ala	Gly	Val	Asp	165	170	175	
Ala	Leu	Val	Lys	Asp	Gly	Glu	Glu	Val	Val	Lys	Gly	Gln	Glu	Leu	Ala	180	185	190	
Pro	Gly	Val	Val	Ser	Arg	Met	Asp	Gly	Val	Gly	Ser	Leu	Pro	Leu	Pro	195	200	205	
Arg	Arg	Val	Arg	Val	Asp	Tyr	Leu	Arg	Lys	Glu	Arg	Ala	Ala	Leu	Arg	210	215	220	
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Val	Leu	Ala	Glu	Leu	Ser	Glu	Pro	Tyr	Leu	Phe	Arg	Ala	Glu	Glu	Ser	245	250	255	
Gly	Val	Val	Glu	Leu	Lys	Asp	Leu	Ala	Glu	Gly	His	Leu	Ile	Tyr	Leu	260	265	270	
Arg	Gln	Glu	Glu	Glu	Val	Val	Ala	Arg	Tyr	Phe	Leu	Pro	Ala	Gly	Met	275	280	285	
Thr	Pro	Leu	Val	Val	Glu	Gly	Glu	Ile	Val	Glu	Val	Gly	Gln	Pro	Leu	290	295	300	
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Glu	Val	Glu	Ala	Glu	Glu	Glu	Gly	Asp	Ser	Val	His	Leu	Thr	Leu	Phe	325	330	335	
Leu	Glu	Trp	Thr	Glu	Pro	Lys	Asp	Tyr	Lys	Val	Ala	Pro	His	Met	Asn	340	345	350	
Val	Ile	Val	Pro	Glu	Gly	Ala	Lys	Val	Gln	Ala	Gly	Glu	Lys	Ile	Val	355	360	365	
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Tyr	Pro	Phe	Glu	Asp	Asp	Val	Glu	Val	Thr	Thr	Gly	Asp	Arg	Val	Ala	405	410	415	
Pro	Gly	Asp	Val	Leu	Ala	Asp	Gly	Gly	Lys	Val	Lys	Ser	Glu	Ile	Tyr	420	425	430	
Gly	Arg	Val	Glu	Val	Asp	Leu	Val	Arg	Asn	Val	Val	Arg	Val	Val	Glu	435	440	445	

Ser Tyr Asp Ile Asp Ala Arg Met Gly Ala Glu Ala Ile Gln Glu Leu
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				885					890					895		
Gln	Glu	Leu	Ile	Gln	Met	Asp	Val	Pro	Gln	Glu	Lys	Asn	Ser	Leu	Lys	
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Asp	Leu	Val	Tyr	Gln	Ala	Phe	Leu	Arg	Leu	Gly	Met	Glu	Lys	Thr	Ala	
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Arg	Leu	Leu	Asp	Ala	Leu	Lys	Tyr	Tyr	Gly	Phe	Thr	Leu	Ser	Thr	Thr	
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 Phe Gln Asn Thr Thr His Val Leu Thr Glu Ala Ala Ile Ala Gly Lys
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 Ile Pro Ala Gly Thr Gly Ser Asp Phe Val Arg Phe Thr Gln Val Val
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 35 40 45
 Lys Glu Thr Phe Pro Ile Glu Glu Gly Asp Lys Gly Lys Gly Gly Leu
 50 55 60

Val	Leu	Asp	Phe	Leu	Glu	Tyr	Arg	Ile	Gly	Asp	Pro	Pro	Phe	Ser	Gln	65	70	75	80
Asp	Glu	Cys	Arg	Glu	Lys	Asp	Leu	Thr	Tyr	Gln	Ala	Pro	Leu	Tyr	Ala	85	90	95	
Arg	Leu	Gln	Leu	Ile	His	Lys	Asp	Thr	Gly	Leu	Ile	Lys	Glu	Asp	Glu	100	105	110	
Val	Phe	Leu	Gly	His	Leu	Pro	Leu	Met	Thr	Glu	Asp	Gly	Ser	Phe	Ile	115	120	125	
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Gly	Val	Tyr	Phe	Thr	Pro	Asp	Pro	Ala	Arg	Pro	Gly	Arg	Tyr	Ile	Ala	145	150	155	160
Ser	Ile	Ile	Pro	Leu	Pro	Lys	Arg	Gly	Pro	Trp	Ile	Asp	Leu	Glu	Val	165	170	175	
Glu	Ala	Ser	Gly	Val	Val	Thr	Met	Lys	Val	Asn	Lys	Arg	Lys	Phe	Pro	180	185	190	
Leu	Val	Leu	Leu	Leu	Arg	Val	Leu	Gly	Tyr	Asp	Gln	Glu	Thr	Leu	Val	195	200	205	
Arg	Glu	Leu	Ser	Ala	Tyr	Gly	Asp	Leu	Val	Gln	Gly	Leu	Leu	Asp	Glu	210	215	220	
Ala	Val	Leu	Ala	Met	Arg	Pro	Glu	Glu	Ala	Met	Val	Arg	Leu	Phe	Thr	225	230	235	240
Leu	Leu	Arg	Pro	Gly	Asp	Pro	Pro	Lys	Lys	Asp	Lys	Ala	Leu	Ala	Tyr	245	250	255	
Leu	Phe	Gly	Leu	Leu	Ala	Asp	Pro	Lys	Arg	Tyr	Asp	Leu	Gly	Glu	Ala	260	265	270	
Gly	Arg	Tyr	Lys	Ala	Glu	Glu	Lys	Leu	Gly	Val	Gly	Leu	Ser	Gly	Arg	275	280	285	
Thr	Leu	Val	Arg	Phe	Glu	Asp	Gly	Glu	Phe	Lys	Asp	Glu	Val	Phe	Leu	290	295	300	
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Pro Ala Lys Leu Val Asn Ser Arg Pro Leu Glu Ala Ala Leu Arg Glu
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 Phe Phe Ser Arg Ser Gln Leu Ser Gln Phe Lys Asp Glu Thr Asn Pro
 385 390 395 400
 Leu Ser Ser Leu Arg His Lys Arg Arg Ile Ser Ala Leu Gly Pro Gly
 405 410 415
 Gly Leu Thr Arg Glu Arg Ala Gly Phe Asp Val Arg Asp Val His Arg
 420 425 430
 Thr His Tyr Gly Arg Ile Cys Pro Val Glu Thr Pro Glu Gly Ala Asn
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 Ile Gly Leu Ile Thr Ser Leu Ala Ala Tyr Ala Arg Val Asp Ala Leu
 450 455 460
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 465 470 475 480
 Glu Glu Val Val Tyr Met Thr Ala Ser Glu Glu Asp Arg Tyr Thr Ile
 485 490 495
 Ala Gln Ala Asn Thr Pro Leu Glu Gly Asp Arg Ile Ala Thr Asp Arg
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 Val Val Ala Arg Arg Arg Gly Glu Pro Val Ile Val Ala Pro Glu Glu
 515 520 525
 Val Glu Phe Met Asp Val Ser Pro Lys Gln Val Phe Ser Leu Asn Thr
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 545 550 555 560
 Gly Ser Asn Met Gln Thr Gln Ala Val Pro Leu Ile Arg Ala Gln Ala
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 Pro Val Val Met Thr Gly Leu Glu Glu Arg Val Val Arg Asp Ser Leu
 580 585 590
 Ala Ala Leu Tyr Ala Glu Glu Asp Gly Glu Val Val Lys Val Asp Gly
 595 600 605
 Thr Arg Ile Ala Val Arg Tyr Glu Asp Gly Arg Leu Val Glu His Pro
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 Leu Arg Arg Tyr Ala Arg Ser Asn Gln Gly Thr Ala Phe Asp Gln Arg
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 Pro Arg Val Arg Val Gly Gln Arg Val Lys Lys Gly Asp Leu Leu Ala
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 Asp Gly Pro Ala Ser Glu Glu Gly Phe Leu Ala Leu Gly Gln Asn Val
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Val	Ile	Ser	Glu	Glu	Leu	Xaa	Xaa	Arg	Asp	Phe	Tyr	Thr	Ser	Ile	His	690	695	700
Ile	Glu	Arg	Tyr	Glu	Ile	Glu	Ala	Arg	Asp	Thr	Lys	Leu	Gly	Pro	Glu	705	710	715
Arg	Ile	Thr	Arg	Asp	Ile	Pro	His	Leu	Ser	Glu	Ala	Ala	Leu	Arg	Asp	725	730	735
Leu	Asp	Glu	Glu	Gly	Ile	Val	Arg	Ile	Gly	Ala	Glu	Val	Lys	Pro	Gly	740	745	750
Asp	Ile	Leu	Val	Gly	Arg	Thr	Ser	Phe	Lys	Gly	Glu	Gln	Glu	Pro	Ser	755	760	765
Pro	Glu	Glu	Arg	Leu	Leu	Arg	Ser	Ile	Phe	Gly	Glu	Lys	Ala	Arg	Asp	770	775	780
Val	Lys	Asp	Thr	Ser	Leu	Arg	Val	Pro	Pro	Gly	Glu	Gly	Gly	Ile	Val	785	790	795
Val	Gly	Arg	Leu	Arg	Leu	Arg	Arg	Gly	Asp	Pro	Gly	Val	Glu	Leu	Lys	805	810	815
Pro	Gly	Val	Arg	Glu	Val	Val	Arg	Val	Phe	Val	Ala	Gln	Lys	Arg	Lys	820	825	830
Leu	Gln	Val	Gly	Asp	Lys	Leu	Ala	Asn	Arg	His	Gly	Asn	Lys	Gly	Val	835	840	845
Val	Ala	Lys	Ile	Leu	Pro	Val	Glu	Asp	Met	Pro	His	Leu	Pro	Asp	Gly	850	855	860
Thr	Pro	Val	Asp	Val	Ile	Leu	Asn	Pro	Leu	Gly	Val	Pro	Ser	Arg	Met	865	870	875
Asn	Leu	Gly	Gln	Ile	Leu	Glu	Thr	His	Leu	Gly	Leu	Ala	Gly	Tyr	Phe	885	890	895
Leu	Gly	Gln	Arg	Tyr	Ile	Ser	Pro	Val	Phe	Asp	Gly	Ala	Thr	Glu	Pro	900	905	910
Glu	Ile	Lys	Glu	Leu	Leu	Ala	Glu	Ala	Phe	Asn	Leu	Tyr	Phe	Gly	Lys	915	920	925
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Ala	Arg	Ala	Glu	Lys	Leu	Gly	Leu	Val	Ser	Pro	Gly	Lys	Ser	Pro	Glu	945	950	955
Glu	Gln	Leu	Lys	Glu	Leu	Phe	Asp	Leu	Gly	Lys	Val	Val	Leu	Tyr	Asp	965	970	975

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 Phe Ser Thr Ile Pro Gly Val Lys Glu Asp Val Val Glu Ile Ile Leu
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35 40 45

Arg Thr Leu Glu Gly Leu Tyr Asp Asp Pro Asn Ala Val Thr Trp Ala
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Xaa Xaa Gly Leu Xaa Xaa Xaa Arg Arg Asn Leu Xaa Ala Xaa Gly Pro
 20 25 30

Gly Gly

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<213> Mycobacterium tuberculosis

<400> 15

Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile Gly Ser Leu
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<213> Mycobacterium tuberculosis

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Asn Met Gln Arg Gln Ala Val
 1 5

<210> 17

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<213> Saccharomyces cerevisiae

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Lys Val Leu Ile Ala Gln
 1 5

<210> 18

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<213> Saccharomyces cerevisiae

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Met Ser Ser Arg Ala Gly Val Ser Gln Val Leu Asn Arg Tyr Thr Tyr
 1 5 10 15

Ser Ser Thr Leu Ser His Leu Arg Arg Thr Asn Thr Pro Ile Gly
 20 25 30

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<213> *Saccharomyces cerevisiae*

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Glu Thr Pro Glu Gly Gln Ala Cys Gly Leu Val Lys Asn Leu
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Ala Met Gly Lys Gln Ala Met
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Lys Val Leu Ile Ala Gln
 1 5

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<213> *Homo sapiens*

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His Gln Ala Arg Ala Gly Val Ser Gln Val Leu Asn Arg Leu Thr Phe
 1 5 10 15

Ala Ser Thr Leu Ser His Leu Arg Arg Leu Asn Ser Pro Ile Gly
 20 25 30

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<213> *Homo sapiens*

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Glu Thr Pro Glu Gly His Ala Val Gly Leu Val Lys Asn Leu
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<213> *Homo sapiens*

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Ala Met Gly Lys Gln Ala Met
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<213> *Drosophila melanogaster*

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Lys Val Leu Ile Ala Gln
1 5

<210> 26

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<213> *Drosophila melanogaster*

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1 5 10 15Ala Ser Thr Leu Ser His Leu Arg Arg Val Asn Ser Pro Ile Gly
20 25 30

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<213> *Drosophila melanogaster*

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Glu Thr Pro Glu Gly Ala Ala Val Gly Leu Val Lys Asn Leu
1 5 10

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<213> *Drosophila melanogaster*

<400> 28

Ala Met Gly Lys Gln Ala Met
1 5

<210> 29

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<213> *Escherichia coli*

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Tyr Trp Ile Val
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polynucleotide sequence

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19